Multiresistant pathogens: The case of non-fermentative Gram-negative bacilli

S215 Changes in classification of glucose-non-fermenting gram-negative bacilli

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Modern taxonomy is polyphasic and incorporates genotypic, phenotypic and phylogenetic markers. Genotypic characteristics are based on analysis of DNA or RNA molecules. rRNA is currently regarded as the optimal target for phylogenetic analysis as it is composed of highly conserved as well as variable domains. At this time direct DNA-sequencing of coding regions for 16S or 23S rRNA is widely performed. Phenotypic procedures include all non-nucleic acid directed approaches, e.g. composition of cell wall or cellular fatty acids, whole cell protein analysis etc.

Recent progress in technology allowed accumulation of new data leading to revisions in taxonomy and nomenclature (Bruckner & Colonna, CID, 1995) in major groups of bacteria. This holds true as well for glucose-non-fermenting gram-negative bacilli, e.g. *Acinetobacter, Pseudomonas* and others. Major reclassifications concern the genus *Pseudomonas*. It was subdivided into five rRNA-DNA-homology groups by Palleroni et al. in 1973. The genus *Pseudomonas* is now restricted to the former rRNA-group I, the species of rRNA-group II were transferred to the new genera *Burkholderia* and *Ralstonia*, rRNA-group III became the family *Comamonadaceae*, rRNA-group IV was transferred to the genus *Brevundimonas*, and rRNA-group V to *Stenotrophomonas* (via *Xanthomonas*).

Recently molecular procedures based on specific signature sequences within the 16S or 23S rRNA have been designed to identify species, e.g. within the genus *Burkholderia*. They improve identification of species difficult to separate by phenotypic procedures. There are, however, examples which demonstrate the limitations of genetic procedures, e.g. to differentiate between the phenotypically distinct species *Burkholderia cepacia* and *B. vietnamiensis*. This underlines the importance of polyphasic taxonomy for valid classification and nomenclature.

S216 Cross-Infection with Multiresistant Pseudomonas, Burkholderia and Other Non-Fermenters in Cystic Fibrosis Patients

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The major Gram-negative pathogens responsible for respiratory infection and mortality in cystic fibrosis (CF) are *Pseudomonas aeruginosa* and *Burkholderia cepacia*. However, *Stenotrophomonas maltophilia* and *Alcaligenes xylosoxidans* and a few other non-fermenting species are emerging as possibly important patogens due to the improved survial of the patients. All these species are increasingly resistant to most of the available antibiotics which are used extensively in CF patients. Difficult-to-treat strains and multiply resistant strains are therefore becoming an increasing problem in CF centres. Unfortunately, cross-infection has been documented with at least *P. aeruginosa* and *B. cepacia* in CF centres, in the wards, in the out-patient clinics, in summer-camps and during social activities such as fitness-classes. Even spread of epidemic strains between centres and between countries and between continents has been observed. Such transmissible strains are often multiply resistant due to the selective pressure imposed by the exttensive use of antibiotics in CF patients. The most effective preventive measure has been the use of cohorte isolation technique and high level of hygine in CF centres and during social activities. The cohorting is based on bacteriological examination of sputum, and e.g. patients culture-positive for *P. aeruginosa* are kept isolated by geography and/or time from culture-negative patients. Social activities such as summer camps are completely avoided in some countries.

S217 Acinetobacter: facts and fears

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The presentation will cover the following facts: Epidemiological significance of cutaneous, pharyngeal and digestive tract colonisation by *Acinetobacter*, survival of *Acinetobacter* on dry surfaces, nosocomial outbreaks, risk factors for nosocomial colonisation, laboratory investigations of outbreaks, antimicrobial susceptibility.

Fears: Why are hospital epidemiologists very much afraid of *Acinetobacter*? Why is it difficult to get rid of these organisms in hospitals when they colonise patients especially in intensive care units? Is there airborne spread of *Acinetobacter*?

S218 Moraxella and Oligella: Ecology and Pathogenicity

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No abstract available.

Gene therapy: Where do we stand?

S219 Retroviruses for Gene Delivery

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We have demonstrated that the sensitivity of retroviruses to human serum is controlled by the expression or alpha 1–3 galactosyl sugar epitopes. We have now made high titre packaging cells producing viruses resistant to human serum. We are also attempting to retarget retroviruses to novel surface receptors using an insertion point in the MLV envelope which allows incorporation of an additional receptor binding domain. Our results with chimeric envelopes expressing ligands or single chain antibodies will be discussed. Finally, our strategies using retroviruses for tumour gene therapy will be presented. These include *ex vivo* modification of tumour cells which are being used in a melanoma vaccine clinical trial and targetting retroviral delivery to tumour cells.

S220 Genetic Approaches for HIV Infection: Promises and Hurdles

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First developed for hereditary disorders, gene therapy is also envisioned for the treatment of oncologic and infectious diesases. In the latter case, the genetic modification of cells is aimed at reducing or ablating the replication of a pathogen, resulting in what has been called an "intracellular immunization". In spite of the recent success of pharmaceutical approaches for the management of HIV-induced disease, currently available antiviral drugs are toxic, costly, and need to be administered for an extremely long time, if not for the patients' entire life. Based on this premise, genetic approaches might represent a valid if only complementary approach for the treatment of HIV infection. The progress made towards meeting this objective, as well as the problems still remaining and their potential solutions, will be discussed.